

From: Steadman, David (AU1652)  
Sent: Wednesday, February 08, 2006 1:18 PM  
To: STIC-Biotech/ChemLib  
Subject: 10/601,011 sequence search request

NAME: David Steadman  
AU: 1656  
Date: 2/8/06  
Office: Remsen 2B05  
Mailbox: Remsen 3C70

RECEIVED  
FEB - 8 2006  
STIC-BIOTECH/CHM LIB  
(STIC)

**Please search the following sequences in commercial databases:**

- 1) amino acids 126-388 of SEQ ID NO:1 against amino acid databases.
- 2) amino acids 126-388 of SEQ ID NO:1 against nucleic acid databases.

*Please save results to diskette.*

Thank you very much.

David J. Steadman, Ph.D.  
Primary Examiner  
Art Unit 1656  
Protein Crystallography and Recombinant Enzymes  
Office: Remsen 2B05  
Mailbox: Remsen 3C70  
Phone: (571) 272-0942

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 12, 2006, 18:56:45 ; Search time 81 Seconds  
 (without alignments)  
 1426.625 Million cell updates/sec

Title: US-10-601-011-1\_COPY\_126\_388  
 Perfect score: 1383  
 Sequence: 1 RQWALEDFEIGRPLGKGKFG.....SQRPMLREVLEHPWITANSS 263

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_21:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*  
 9: geneseqp2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%	Query				
No.	Score	Match	Length	DB	ID	Description	
1	1383	100.0	282	9	ADZ47152	Adz47152 Human aur	
2	1383	100.0	403	2	AAW18084	Aaw18084 Human Aur	
3	1383	100.0	403	2	AAY22476	Aay22476 Human AUR	
4	1383	100.0	403	4	AAG67614	Aag67614 Amino aci	
5	1383	100.0	403	4	AAG67435	Aag67435 Amino aci	
6	1383	100.0	403	6	ABP97367	Abp97367 Human ser	
7	1383	100.0	403	6	ABP97366	Abp97366 Human ser	
8	1383	100.0	403	6	ABR48160	Abr48160 Human bla	

9	1383	100.0	403	7	ADF61840	Adf61840 Human ser
10	1383	100.0	403	7	ADN39888	Adn39888 Cancer/an
11	1383	100.0	403	8	ADE15337	Ade15337 Truncated
12	1383	100.0	403	8	ADH59556	Adh59556 Monoclonal
13	1383	100.0	403	8	ADK67720	Adk67720 Human mod
14	1383	100.0	403	8	ADM72205	Adm72205 Human TAS
15	1383	100.0	403	8	ADQ89832	Adq89832 Antagonis
16	1383	100.0	403	8	ADR05174	Adr05174 Human GTP
17	1383	100.0	403	8	ADU06485	Adu06485 Novel bro
18	1383	100.0	403	9	ADW15992	Adw15992 Human aur
19	1383	100.0	403	9	ADX06369	Adx06369 Cyclin-de
20	1383	100.0	403	9	ADY15254	Ady15254 PRO polyp
21	1383	100.0	403	9	AEB87732	Aeb87732 Human aur
22	1383	100.0	420	5	ABP41958	Abp41958 Human ova
23	1383	100.0	461	8	ADX97535	Adx97535 Pancreati
24	1377	99.6	300	6	ABP97473	Abp97473 Truncated
25	1377	99.6	309	6	ABP97472	Abp97472 Truncated
26	1377	99.6	319	6	ABP97470	Abp97470 Truncated
27	1374	99.3	403	7	ADJ31727	Adj31727 Human mit
28	1367.5	98.9	402	9	ADZ64605	Adz64605 Kinase do
29	1332	96.3	402	7	ABR61579	Abr61579 Human HsA
30	1332	96.3	402	7	ADD89969	Add89969 Human can
31	1332	96.3	402	8	ADU06504	Adu06504 Novel bro
32	1332	96.3	402	9	ADX06367	Adx06367 Cyclin-de
33	1332	96.3	402	9	ADY15914	Ady15914 PRO polyp
34	1303.5	94.3	320	9	ADY85555	Ady85555 Catalytic
35	1284	92.8	403	5	AAO18740	Aao18740 Human NOV
36	1174	84.9	279	9	ADZ47153	Adz47153 Clawed fr
37	1125	81.3	267	9	ADZ47154	Adz47154 Takifugu
38	1047	75.7	280	9	ADZ47158	Adz47158 Clawed fr
39	1044	75.5	279	9	ADZ47157	Adz47157 Human aur
40	1044	75.5	336	8	ADX97574	Adx97574 Pancreati
41	1044	75.5	344	2	AAW18083	Aaw18083 Human Aur
42	1044	75.5	344	2	AAY22475	Aay22475 Human AUR
43	1044	75.5	344	4	AAG67615	Aag67615 Amino aci
44	1044	75.5	344	4	AAG67436	Aag67436 Amino aci
45	1044	75.5	344	6	ABR48188	Abr48188 Human bla

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OM protein - protein search, using sw model

Run on: February 12, 2006, 19:03:40 ; Search time 174 Seconds  
(without alignments)  
631.547 Million cell updates/sec

Title: US-10-601-011-1\_COPY\_126\_388  
Perfect score: 1383  
Sequence: 1 RQWALEDFEIGRPLGKGKFG.....SQRPMLREVLEHPWITANSS 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%				Description
	No.	Score	Match	Length	ID		
1	1383	100.0	322	4	US-10-664-421-125		Sequence 125, App
2	1383	100.0	403	3	US-09-012-135A-4		Sequence 4, Appli
3	1383	100.0	403	3	US-09-784-332-4		Sequence 4, Appli
4	1383	100.0	403	4	US-10-060-065-12		Sequence 12, Appl
5	1383	100.0	403	4	US-10-059-585-33		Sequence 33, Appl
6	1383	100.0	403	4	US-10-209-324-2		Sequence 2, Appli
7	1383	100.0	403	4	US-10-295-027-1206		Sequence 1206, Ap
8	1383	100.0	403	4	US-10-087-684-47		Sequence 47, Appl
9	1383	100.0	403	4	US-10-087-684-48		Sequence 48, Appl
10	1383	100.0	403	4	US-10-087-684-49		Sequence 49, Appl
11	1383	100.0	403	4	US-10-218-779-47		Sequence 47, Appl

12	1383	100.0	403	4	US-10-218-779-48	Sequence 48, Appl
13	1383	100.0	403	4	US-10-218-779-49	Sequence 49, Appl
14	1383	100.0	403	4	US-10-188-832-35	Sequence 35, Appl
15	1383	100.0	403	5	US-10-751-736-65	Sequence 65, Appl
16	1383	100.0	403	5	US-10-734-126-4	Sequence 4, Appli
17	1383	100.0	403	5	US-10-781-581-187	Sequence 187, App
18	1383	100.0	403	5	US-10-979-375-1	Sequence 1, Appli
19	1383	100.0	403	5	US-10-745-237-262	Sequence 262, App
20	1383	100.0	403	5	US-10-965-313-1	Sequence 1, Appli
21	1383	100.0	403	6	US-11-037-713-2	Sequence 2, Appli
22	1383	100.0	403	6	US-11-092-809-1	Sequence 1, Appli
23	1383	100.0	403	6	US-11-092-863-1	Sequence 1, Appli
24	1383	100.0	420	4	US-10-264-049-3090	Sequence 3090, Ap
25	1374	99.3	403	4	US-10-026-021-7	Sequence 7, Appli
26	1374	99.3	403	4	US-10-087-684-50	Sequence 50, Appl
27	1374	99.3	403	4	US-10-218-779-50	Sequence 50, Appl
28	1332	96.3	321	5	US-10-941-635-127	Sequence 127, App
29	1332	96.3	402	4	US-10-087-684-51	Sequence 51, Appl
30	1332	96.3	402	4	US-10-218-779-51	Sequence 51, Appl
31	1332	96.3	402	5	US-10-509-599-14	Sequence 14, Appl
32	1284	92.8	403	4	US-10-087-684-14	Sequence 14, Appl
33	1284	92.8	403	4	US-10-218-779-14	Sequence 14, Appl
34	1044	75.5	344	3	US-09-012-135A-3	Sequence 3, Appli
35	1044	75.5	344	3	US-09-784-332-3	Sequence 3, Appli
36	1044	75.5	344	4	US-10-060-065-13	Sequence 13, Appl
37	1044	75.5	344	4	US-10-059-585-34	Sequence 34, Appl
38	1044	75.5	344	4	US-10-171-311-214	Sequence 214, App
39	1044	75.5	344	4	US-10-295-027-203	Sequence 203, App
40	1044	75.5	344	4	US-10-173-999-101	Sequence 101, App
41	1044	75.5	344	4	US-10-188-832-93	Sequence 93, Appl
42	1044	75.5	344	5	US-10-734-126-3	Sequence 3, Appli
43	1044	75.5	344	5	US-10-745-237-264	Sequence 264, App
44	1044	75.5	344	5	US-10-965-313-2	Sequence 2, Appli
45	1044	75.5	344	6	US-11-037-713-30	Sequence 30, Appl

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 14, 2006, 20:29:25 ; Search time 3993 Seconds  
(without alignments)  
3744.009 Million cell updates/sec

Title: US-10-601-011-1\_COPY\_126\_388  
Perfect score: 1383  
Sequence: 1 RQWALEDFFEIGRPLGKGKFG.....SQRPMLREVLEHPWITANSS 263

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10601011/runat\_12022006\_150911\_13333/app\_query.fasta\_1  
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p  
-USER=US10601011\_@CGN\_1\_1\_7415\_@runat\_12022006\_150911\_13333 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*

13: gb\_vi:\*  
 14: gb\_htg:\*  
 15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	Query					Description
	No.	Score	Match Length	DB	ID	
c	1	1383	100.0	1212	8	AF008551 Homo sapi
	2	1383	100.0	1212	11	AY335576 Synthetic
	3	1383	100.0	1212	11	AY892410 Synthetic
	4	1383	100.0	1212	11	BT008056 Synthetic
	5	1383	100.0	2024	8	BC006423 Homo sapi
	6	1383	100.0	2064	10	BV177260 sqnm93669
	7	1383	100.0	2120	8	BC002499 Homo sapi
	8	1383	100.0	2121	6	CS119570 Sequence
	9	1383	100.0	2128	8	BC001280 Homo sapi
	10	1383	100.0	2135	6	CS119568 Sequence
	11	1383	100.0	2169	8	BC027464 Homo sapi
	12	1383	100.0	2198	6	AR078203 Sequence
	13	1383	100.0	2198	6	AR081975 Sequence
	14	1383	100.0	2198	6	AR139681 Sequence
	15	1383	100.0	2198	6	BD140128 Diagnosis
	16	1383	100.0	2198	6	AR491644 Sequence
	17	1383	100.0	2198	6	AR630705 Sequence
	18	1383	100.0	2231	6	CS119569 Sequence
	19	1383	100.0	2237	6	CQ728025 Sequence
	20	1383	100.0	2237	6	AX281843 Sequence
	21	1383	100.0	2245	6	CS119567 Sequence
	22	1383	100.0	2253	6	CQ759659 Sequence
	23	1383	100.0	2253	6	CQ894702 Sequence
	24	1383	100.0	2253	6	CQ981365 Sequence
	25	1383	100.0	2253	6	CS031553 Sequence
	26	1383	100.0	2253	6	CS040505 Sequence
	27	1383	100.0	2253	6	CS118077 Sequence
	28	1383	100.0	2253	6	AR198495 Sequence
	29	1383	100.0	2253	8	AF011468 Homo sapi
c	30	1383	100.0	2284	6	CQ414603 Sequence
	31	1383	100.0	2346	6	CS119565 Sequence
	32	1383	100.0	2347	6	AR648112 Sequence
	33	1383	100.0	2554	6	CS119566 Sequence
	34	1363	98.6	2148	6	AX281842 Sequence
	35	1349	97.5	1934	8	AB168134 Macaca fa
	36	1334.5	96.5	1218	4	AB196773 Sus scrof
	37	1332	96.3	1209	6	CQ847956 Sequence
	38	1332	96.3	1209	6	AX934319 Sequence
	39	1332	96.3	2033	6	CQ981384 Sequence
	40	1332	96.3	2033	6	CS032213 Sequence
	41	1332	96.3	2033	6	CS041165 Sequence
	42	1332	96.3	2033	6	AR198502 Sequence
	43	1332	96.3	2033	6	AX925606 Sequence
	44	1332	96.3	2033	8	D84212 Homo sapien

45 1310 94.7 1194 9 AF537333

AF537333 Rattus no



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 14, 2006, 21:16:44 ; Search time 187 Seconds  
(without alignments)  
2499.993 Million cell updates/sec

Title: US-10-601-011-1\_COPY\_126\_388  
Perfect score: 1383  
Sequence: 1 RQWALED FEIGRPLGKGKFG.....SQRPMLREVLEHPWITANSS 263

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10601011/runat\_12022006\_150916\_13432/app\_query.fasta\_1  
-DB=Issued\_Patents\_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-HOST=abss06p -USER=US10601011 @CGN\_1\_1\_290 @runat\_12022006\_150916\_13432  
-NCPU=6 -ICPU=3 -NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/1\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/H\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/ina/PP\_COMB.seq:\*  
8: /cgn2\_6/ptodata/1/ina/RE\_COMB.seq:\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1383	100.0	2198	2	US-08-755-728-2	Sequence 2, Appli
2	1383	100.0	2198	2	US-08-974-655-2	Sequence 2, Appli
3	1383	100.0	2198	3	US-09-283-011-2	Sequence 2, Appli
4	1383	100.0	2198	3	US-09-012-135A-2	Sequence 2, Appli
5	1383	100.0	2198	3	US-09-784-332-2	Sequence 2, Appli
6	1383	100.0	2237	3	US-09-949-016-4590	Sequence 4590, Ap
7	1383	100.0	2237	3	US-09-949-016-4591	Sequence 4591, Ap
8	1383	100.0	2253	3	US-09-660-925B-3	Sequence 3, Appli
9	1383	100.0	2347	3	US-10-209-324-1	Sequence 1, Appli
10	1332	96.3	2033	3	US-09-660-925B-10	Sequence 10, Appl
11	1044	75.5	1224	3	US-09-949-016-3955	Sequence 3955, Ap
12	1044	75.5	1244	2	US-08-755-728-1	Sequence 1, Appli
13	1044	75.5	1244	2	US-08-974-655-1	Sequence 1, Appli
14	1044	75.5	1244	3	US-09-283-011-1	Sequence 1, Appli
15	1044	75.5	1244	3	US-09-012-135A-1	Sequence 1, Appli
16	1044	75.5	1244	3	US-09-784-332-1	Sequence 1, Appli
17	1032.5	74.7	1281	2	US-09-016-000-7	Sequence 7, Appli
18	1029	74.4	1815	3	US-09-485-534-3	Sequence 3, Appli
19	685	49.5	9822	3	US-09-949-016-15697	Sequence 15697, A
20	666.5	48.2	1533	3	US-09-248-796A-4410	Sequence 4410, Ap
21	528	38.2	747	3	US-09-270-767-15286	Sequence 15286, A
22	527	38.1	26867	3	US-09-949-016-16332	Sequence 16332, A
23	527	38.1	26867	3	US-09-949-016-16333	Sequence 16333, A
24	505.5	36.6	3937	3	US-09-620-312D-280	Sequence 280, App
25	501.5	36.3	1453	2	US-08-252-995D-1	Sequence 1, Appli
26	501.5	36.3	1453	2	US-08-834-108-1	Sequence 1, Appli
27	501.5	36.3	1600	2	US-08-252-995D-5	Sequence 5, Appli
28	501.5	36.3	1600	2	US-08-834-108-5	Sequence 5, Appli
29	501.5	36.3	3447	2	US-08-252-995D-3	Sequence 3, Appli
30	501.5	36.3	3447	2	US-08-834-108-3	Sequence 3, Appli
31	480.5	34.7	781	3	US-09-533-559-7482	Sequence 7482, Ap
32	468	33.8	1194	3	US-09-487-558B-399	Sequence 399, App
33	466	33.7	1197	3	US-09-487-558B-403	Sequence 403, App
34	452	32.7	1929	3	US-09-359-161-4	Sequence 4, Appli
35	444	32.1	3857	3	US-10-464-939-1	Sequence 1, Appli
36	444	32.1	4790	3	US-10-464-939-3	Sequence 3, Appli
37	443	32.0	1143	3	US-09-487-558B-401	Sequence 401, App
38	437.5	31.6	993	3	US-09-248-796A-4394	Sequence 4394, Ap
39	435.5	31.5	1732	3	US-09-430-564-1	Sequence 1, Appli
40	435.5	31.5	1816	3	US-09-762-258-1	Sequence 1, Appli
41	433.5	31.3	2698	2	US-08-677-298-1	Sequence 1, Appli
42	433.5	31.3	2912	3	US-09-949-016-2363	Sequence 2363, Ap
43	433.5	31.3	2914	3	US-09-949-016-343	Sequence 343, App
44	432	31.2	1212	3	US-09-248-796A-6416	Sequence 6416, Ap
45	430	31.1	1539	3	US-09-633-328B-1	Sequence 1, Appli

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 14, 2006, 21:21:44 ; Search time 1404 Seconds  
(without alignments)  
168.433 Million cell updates/sec

Title: US-10-601-011-1\_COPY\_126\_388  
Perfect score: 1383  
Sequence: 1 RQWALEDFEIGRPLGKGKFG.....SQRPMLREVLEHPWITANSS 263

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 6240305 seqs, 449581930 residues

Total number of hits satisfying chosen parameters: 12480610

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10601011/runat\_12022006\_150920\_13536/app\_query.fasta\_1  
-DB=Published\_Applications\_NA\_New -QFMT=fastap -SUFFIX=rnpbn -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abss06p  
-USER=US10601011\_@CGN\_1\_1\_335\_@runat\_12022006\_150920\_13536 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA\_New:\*  
1: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq1:\*  
8: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq2:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq3:\*  
11: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq4:\*

12: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1383	100.0	2253	7	US-10-770-726-39	Sequence 39, Appl	
2	1383	100.0	2253	11	US-11-000-688-124	Sequence 124, App	
3	1383	100.0	2347	7	US-10-770-726-41	Sequence 41, Appl	
4	1332	96.3	2033	7	US-10-523-477-4	Sequence 4, Appli	
5	1044	75.5	1224	7	US-10-523-477-2	Sequence 2, Appli	
6	1044	75.5	1224	7	US-10-770-726-40	Sequence 40, Appl	
7	1044	75.5	1224	11	US-11-136-815A-4	Sequence 4, Appli	
8	1004	72.6	1327	7	US-10-523-477-3	Sequence 3, Appli	
9	508.5	36.8	3331	7	US-10-770-726-42	Sequence 42, Appl	
10	435.5	31.5	1680	7	US-10-770-726-37	Sequence 37, Appl	
11	433.5	31.3	3394	7	US-10-995-561-364	Sequence 364, App	
12	433.5	31.3	3442	7	US-10-995-561-361	Sequence 361, App	
13	433.5	31.3	3466	7	US-10-995-561-363	Sequence 363, App	
14	433.5	31.3	3487	7	US-10-995-561-359	Sequence 359, App	
15	433.5	31.3	3514	7	US-10-995-561-360	Sequence 360, App	
16	428	30.9	1891	11	US-11-000-688-55	Sequence 55, Appl	
17	421.5	30.5	1800	11	US-11-136-527-3715	Sequence 3715, Ap	
18	421.5	30.5	2301	11	US-11-136-527-3070	Sequence 3070, Ap	
19	421.5	30.5	2346	11	US-11-117-013-3	Sequence 3, Appli	
20	421.5	30.5	2346	11	US-11-000-688-1538	Sequence 1538, Ap	
21	421	30.4	2972	11	US-11-169-041-72	Sequence 72, Appl	
22	419.5	30.3	2572	11	US-11-136-527-2589	Sequence 2589, Ap	
23	419	30.3	3511	7	US-10-995-561-362	Sequence 362, App	
24	415.5	30.0	2301	11	US-11-151-601-9	Sequence 9, Appli	
25	415.5	30.0	3552	11	US-11-151-601-7	Sequence 7, Appli	
26	414	29.9	2213	7	US-10-770-726-31	Sequence 31, Appl	
27	409	29.6	2190	7	US-10-947-249-104	Sequence 104, App	
28	405.5	29.3	2615	11	US-11-136-527-2878	Sequence 2878, Ap	
29	404	29.2	1915	11	US-11-136-527-2876	Sequence 2876, Ap	
30	403	29.1	1400	11	US-11-136-527-7767	Sequence 7767, Ap	
31	403	29.1	1402	11	US-11-136-527-3671	Sequence 3671, Ap	
32	403	29.1	1442	11	US-11-136-527-1916	Sequence 1916, Ap	
33	402	29.1	3144	11	US-11-136-527-2887	Sequence 2887, Ap	
34	401.5	29.0	1715	7	US-10-947-249-56	Sequence 56, Appl	
c 35	401.5	29.0	3206	7	US-10-821-234-306	Sequence 306, App	
36	401	29.0	2226	11	US-11-136-527-3162	Sequence 3162, Ap	
37	401	29.0	4278	11	US-11-128-061-532	Sequence 532, App	
38	401	29.0	4278	11	US-11-128-049-532	Sequence 532, App	
39	400	28.9	2902	11	US-11-241-056-4	Sequence 4, Appli	
c 40	400	28.9	35893	7	US-10-860-436-2	Sequence 2, Appli	
41	399	28.9	1122	11	US-11-136-527-1805	Sequence 1805, Ap	
42	399	28.9	2685	11	US-11-000-688-270	Sequence 270, App	
43	398.5	28.8	1618	11	US-11-136-527-2397	Sequence 2397, Ap	
44	397	28.7	2312	11	US-11-136-527-3389	Sequence 3389, Ap	
45	396.5	28.7	2349	11	US-11-136-527-2338	Sequence 2338, Ap	

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 14, 2006, 20:38:26 ; Search time 3735 Seconds  
(without alignments)  
3294.512 Million cell updates/sec

Title: US-10-601-011-1\_COPY\_126\_388  
Perfect score: 1383  
Sequence: 1 RQWALEDIFEIGRPLGKGKFG.....SQRPMLREVLEHPWITANSS 263

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10601011/runat\_12022006\_150913\_13375/app\_query.fasta\_1  
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p  
-USER=US10601011\_@CGN\_1\_1\_8010\_@runat\_12022006\_150913\_13375 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_htc:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gss1:\*  
10: gb\_gss2:\*  
11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	% Query					Description
	No.	Score	Match Length DB	ID		
c	1	1383	100.0	1212	11 DQ050151	DQ050151 Homo sapi
	2	1383	100.0	1841	4 CR616247	CR616247 full-leng
	3	1383	100.0	1992	4 CR621289	CR621289 full-leng
	4	1383	100.0	2025	4 CR611278	CR611278 full-leng
	5	1365	98.7	793	8 CX782148	CX782148 HESC3_12_
	6	1322	95.6	811	1 AU124034	AU124034 AU124034
	7	1320.5	95.5	930	5 BX372079	BX372079 BX372079
	8	1316	95.2	1626	4 BC086984	BC086984 Rattus no
	9	1309	94.6	961	5 BQ685975	BQ685975 AGENCOURT
	10	1305	94.4	1843	4 AK085861	AK085861 Mus muscu
	11	1294	93.6	1852	4 AK077513	AK077513 Mus muscu
	12	1274	92.1	855	6 CA488875	CA488875 AGENCOURT
	13	1264	91.4	1923	4 BC050630	BC050630 Homo sapi
	14	1208	87.3	720	7 CN273685	CN273685 170006008
	15	1177	85.1	854	8 CX747442	CX747442 JGI_ANHP4
	16	1172	84.7	834	8 CX873538	CX873538 HESC4_82_
	17	1166	84.3	696	7 CN791002	CN791002 4125663 B
	18	1158	83.7	883	6 CA971494	CA971494 AGENCOURT
	19	1131.5	81.8	1203	5 BU510028	BU510028 AGENCOURT
	20	1118.5	80.9	850	7 CK023559	CK023559 AGENCOURT
	21	1118	80.8	936	5 BU915671	BU915671 AGENCOURT
	22	1117	80.8	838	8 CX219837	CX219837 MNS35076
	23	1100.5	79.6	1055	2 BG027828	BG027828 602294784
	24	1100	79.5	736	5 BU210010	BU210010 602906028
	25	1090	78.8	1010	2 BG027837	BG027837 602294795
	26	1087	78.6	635	2 BE299015	BE299015 601119568
	27	1087	78.6	730	1 AW957623	AW957623 EST369693
	28	1045	75.6	911	5 BU111086	BU111086 603127273
	29	1043	75.4	978	4 CR591471	CR591471 full-leng
	30	1043	75.4	1162	4 CR604968	CR604968 full-leng
	31	1043	75.4	1199	4 CR600836	CR600836 full-leng
	32	1043	75.4	1199	4 CR603941	CR603941 full-leng
	33	1043	75.4	1227	4 CR605805	CR605805 full-leng
	34	1042.5	75.4	859	2 BG290257	BG290257 602384959
	35	1036	74.9	731	7 CR370688	CR370688 CR370688
	36	1036	74.9	747	5 BX304728	BX304728 BX304728
	37	1031	74.5	1923	4 AK075951	AK075951 Mus muscu
	38	1020	73.8	607	2 BG077290	BG077290 H3013F02-
	39	1017	73.5	826	10 AY421575	AY421575 Homo sapi
	40	1016	73.5	810	8 DN510979	DN510979 HL02021B1
	41	1015.5	73.4	1065	5 BX425271	BX425271 BX425271
	42	1013.5	73.3	890	5 BU105061	BU105061 603007034
	43	1011	73.1	890	8 DN110878	DN110878 1109950 M
	44	1007	72.8	674	5 BX846885	BX846885 BX846885
	45	1004	72.6	784	8 CX232498	CX232498 MBM12224

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OM protein - protein search, using sw model

Run on: February 12, 2006, 19:02:55 ; Search time 47 Seconds  
 (without alignments)  
 462.632 Million cell updates/sec

Title: US-10-601-011-1\_COPY\_126\_388  
 Perfect score: 1383  
 Sequence: 1 RQWALEDFFEIGRPLGKGKFG.....SQRPMLREVLEHPWITANSS 263

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/1/iaa/5\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/1/iaa/6\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/iaa/H\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/RE\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1383	100.0	403	1	US-08-755-728-4	Sequence 4, Appli
2	1383	100.0	403	1	US-08-974-655-4	Sequence 4, Appli
3	1383	100.0	403	2	US-09-283-011-4	Sequence 4, Appli
4	1383	100.0	403	2	US-09-012-135A-4	Sequence 4, Appli
5	1383	100.0	403	2	US-09-784-332-4	Sequence 4, Appli
6	1383	100.0	403	2	US-10-209-324-2	Sequence 2, Appli
7	1383	100.0	488	2	US-09-949-016-10461	Sequence 10461, A
8	1383	100.0	488	2	US-09-949-016-10462	Sequence 10462, A
9	1044	75.5	344	1	US-08-755-728-3	Sequence 3, Appli
10	1044	75.5	344	1	US-08-974-655-3	Sequence 3, Appli
11	1044	75.5	344	2	US-09-283-011-3	Sequence 3, Appli

12	1044	75.5	344	2	US-09-012-135A-3	Sequence 3, Appli
13	1044	75.5	344	2	US-09-784-332-3	Sequence 3, Appli
14	1044	75.5	363	2	US-09-949-016-9826	Sequence 9826, Ap
15	1032.5	74.7	347	1	US-09-016-000-1	Sequence 1, Appli
16	1029	74.4	343	2	US-09-485-534-4	Sequence 4, Appli
17	891	64.4	436	2	US-09-485-534-18	Sequence 18, Appl
18	701.5	50.7	412	2	US-09-485-534-19	Sequence 19, Appl
19	666.5	48.2	510	2	US-09-248-796A-18513	Sequence 18513, A
20	501.5	36.3	273	1	US-08-252-995D-10	Sequence 10, Appl
21	501.5	36.3	273	1	US-08-834-108-10	Sequence 10, Appl
22	501.5	36.3	416	1	US-08-252-995D-2	Sequence 2, Appli
23	501.5	36.3	416	1	US-08-834-108-2	Sequence 2, Appli
24	501.5	36.3	464	1	US-08-252-995D-6	Sequence 6, Appli
25	501.5	36.3	464	1	US-08-834-108-6	Sequence 6, Appli
26	501.5	36.3	925	1	US-08-252-995D-4	Sequence 4, Appli
27	501.5	36.3	925	1	US-08-834-108-4	Sequence 4, Appli
28	497.5	36.0	256	2	US-09-964-956-72	Sequence 72, Appl
29	481.5	34.8	256	2	US-09-964-956-74	Sequence 74, Appl
30	474	34.3	260	1	US-07-857-224B-6	Sequence 6, Appli
31	468	33.8	397	2	US-09-487-558B-400	Sequence 400, App
32	466	33.7	398	2	US-09-538-092-501	Sequence 501, App
33	466	33.7	398	2	US-09-487-558B-404	Sequence 404, App
34	457	33.0	227	2	US-09-270-767-46850	Sequence 46850, A
35	453.5	32.8	446	2	US-09-824-735-2	Sequence 2, Appli
36	453	32.8	260	1	US-07-857-224B-8	Sequence 8, Appli
37	447	32.3	258	1	US-07-857-224B-5	Sequence 5, Appli
38	445	32.2	511	2	US-09-633-328B-4	Sequence 4, Appli
39	444	32.1	832	2	US-10-464-939-2	Sequence 2, Appli
40	444	32.1	1058	2	US-10-464-939-4	Sequence 4, Appli
41	443	32.0	380	2	US-09-487-558B-402	Sequence 402, App
42	437.5	31.6	330	2	US-09-248-796A-18497	Sequence 18497, A
43	437	31.6	260	1	US-07-857-224B-7	Sequence 7, Appli
44	435.5	31.5	268	2	US-09-430-564-12	Sequence 12, Appl
45	435.5	31.5	482	2	US-09-430-564-2	Sequence 2, Appli



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OM protein - protein search, using sw model

Run on: February 12, 2006, 19:04:35 ; Search time 16 Seconds  
(without alignments)  
215.702 Million cell updates/sec

Title: US-10-601-011-1\_COPY\_126\_388  
Perfect score: 1383  
Sequence: 1 RQWALED FEIGRPLGKGKFG.....SQRPMLREVLEHPWITANSS 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1383	100.0	403	6	US-10-523-477-11	Sequence 11, Appl
2	1383	100.0	403	6	US-10-770-726-83	Sequence 83, Appl
3	1383	100.0	403	6	US-10-770-726-85	Sequence 85, Appl
4	1383	100.0	403	7	US-11-109-156-12	Sequence 12, Appl
5	1383	100.0	403	7	US-11-092-168-1	Sequence 1, Appli
6	1044	75.5	344	6	US-10-523-477-9	Sequence 9, Appli
7	1044	75.5	344	6	US-10-770-726-84	Sequence 84, Appl
8	1044	75.5	344	7	US-11-109-156-13	Sequence 13, Appl
9	1044	75.5	344	7	US-11-092-168-2	Sequence 2, Appli

10	1004	72.6	275	6	US-10-523-477-10	Sequence 10, Appl
11	508.5	36.8	970	6	US-10-770-726-86	Sequence 86, Appl
12	497.5	36.0	256	6	US-10-877-346-72	Sequence 72, Appl
13	497.5	36.0	256	7	US-11-113-424-183	Sequence 183, App
14	481.5	34.8	256	6	US-10-877-346-74	Sequence 74, Appl
15	466	33.7	398	7	US-11-132-142-7	Sequence 7, Appli
16	445	32.2	381	7	US-11-132-142-9	Sequence 9, Appli
17	435.5	31.5	480	7	US-11-132-142-6	Sequence 6, Appli
18	435.5	31.5	495	6	US-10-770-726-81	Sequence 81, Appl
19	434	31.4	515	7	US-11-132-142-8	Sequence 8, Appli
20	433.5	31.3	713	6	US-10-995-561-881	Sequence 881, App
21	433.5	31.3	729	6	US-10-995-561-878	Sequence 878, App
22	433.5	31.3	737	6	US-10-995-561-880	Sequence 880, App
23	433.5	31.3	744	6	US-10-995-561-876	Sequence 876, App
24	433.5	31.3	753	6	US-10-995-561-877	Sequence 877, App
25	423	30.6	353	7	US-11-132-142-11	Sequence 11, Appl
26	421	30.4	685	7	US-11-169-041-194	Sequence 194, App
27	419	30.3	752	6	US-10-995-561-879	Sequence 879, App
28	416	30.1	462	7	US-11-132-142-10	Sequence 10, Appl
29	415.5	30.0	766	7	US-11-151-601-8	Sequence 8, Appli
30	414	29.9	603	6	US-10-770-726-75	Sequence 75, Appl
31	412	29.8	277	7	US-11-151-601-4	Sequence 4, Appli
32	412	29.8	351	7	US-11-132-142-13	Sequence 13, Appl
33	411	29.7	548	7	US-11-132-142-5	Sequence 5, Appli
34	410.5	29.7	278	6	US-10-055-877-149	Sequence 149, App
35	410.5	29.7	278	7	US-11-103-065-4	Sequence 4, Appli
36	410.5	29.7	278	7	US-11-151-601-10	Sequence 10, Appl
37	409	29.6	740	6	US-10-878-556A-129	Sequence 129, App
38	401.5	29.0	543	6	US-10-821-234-1158	Sequence 1158, Ap
39	401	29.0	343	7	US-11-092-168-3	Sequence 3, Appli
40	400	28.9	631	7	US-11-241-056-11	Sequence 11, Appl
41	399	28.9	332	6	US-10-497-767-3	Sequence 3, Appli
42	399	28.9	351	7	US-11-132-142-14	Sequence 14, Appl
43	396	28.6	395	7	US-11-132-142-12	Sequence 12, Appl
44	393	28.4	350	6	US-10-497-767-4	Sequence 4, Appli
45	390	28.2	514	7	US-11-125-295-2	Sequence 2, Appli

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 14, 2006, 20:22:30 ; Search time 517 Seconds  
(without alignments)  
3390.356 Million cell updates/sec

Title: US-10-601-011-1\_COPY\_126\_388  
Perfect score: 1383  
Sequence: 1 RQWALEDIFEIGRPLGKGKFG.....SQRPMLREVLEHPWITANSS 263

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+\_p2n.model -DEV=xlp  
-Q=/abss/ABSSWEB\_spool/US10601011/runat\_12022006\_150910\_13321/app\_query.fasta\_1  
-DB=N\_Geneseq -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss05p  
-USER=US10601011\_@CGN\_1\_1\_1096\_@runat\_12022006\_150910\_13321 -NCPUs=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N\_Geneseq\_21:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*

13: geneseqn2004bs:\*

14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	1383	100.0	2005	10	ADF61839	Adf61839 Human ser
	2	1383	100.0	2070	6	ABQ55035	Abq55035 Human ova
	3	1383	100.0	2146	8	ACA03962	Aca03962 cDNA down
	4	1383	100.0	2183	13	ADT90062	Adt90062 Human gen
	5	1383	100.0	2198	2	AAT67290	Aat67290 Human Aur
	6	1383	100.0	2198	2	AAX99725	Aax99725 Human AUR
	7	1383	100.0	2237	6	AAS94997	Aas94997 Human DNA
	8	1383	100.0	2253	6	ABK64863	Abk64863 DNA encod
	9	1383	100.0	2253	8	ACC50970	Acc50970 Human bla
	10	1383	100.0	2253	10	ADG89375	Adg89375 Cancer de
	11	1383	100.0	2253	11	ADN39671	Adn39671 Cancer/an
	12	1383	100.0	2253	12	ADH59555	Adh59555 DNA seque
	13	1383	100.0	2253	12	ADM72204	Adm72204 Human TAS
	14	1383	100.0	2253	13	ADR25068	Adr25068 Breast ca
	15	1383	100.0	2253	13	ADT89948	Adt89948 Human gen
	16	1383	100.0	2253	13	ADT90311	Adt90311 Human gen
	17	1383	100.0	2253	13	ADT90574	Adt90574 Human gen
	18	1383	100.0	2253	13	ADT90607	Adt90607 Human gen
	19	1383	100.0	2253	13	ADT90179	Adt90179 Human gen
	20	1383	100.0	2253	13	ADU05998	Adu05998 Novel bro
	21	1383	100.0	2253	13	ADX97464	Adx97464 Pancreati
	22	1383	100.0	2253	14	ADX06368	Adx06368 Cyclin-de
	23	1383	100.0	2253	14	ADY15253	Ady15253 DNA encod
	24	1383	100.0	2253	14	ADY61799	Ady61799 Human gen
	25	1383	100.0	2283	11	ACN89131	Acn89131 Breast ca
c	26	1383	100.0	2284	5	ADL63462	Adl63462 Human ova
	27	1383	100.0	2346	13	ADR05175	Adr05175 Human GTP
	28	1383	100.0	2347	10	ABZ75005	Abz75005 Human ser
	29	1383	100.0	2347	10	ABZ75006	Abz75006 Human ser
	30	1383	100.0	2347	13	ACN40798	Acn40798 Tumour-as
	31	1363	98.6	2148	6	AAS94996	Aas94996 Human DNA
	32	1332	96.3	1209	10	ACF58068	Acf58068 Human HsA
	33	1332	96.3	1209	13	ADQ89831	Adq89831 Antagonis
	34	1332	96.3	2033	6	ABK64870	Abk64870 DNA encod
	35	1332	96.3	2033	10	ADD89968	Add89968 Human can
	36	1332	96.3	2033	12	ADK67713	Adk67713 Human mod
	37	1332	96.3	2033	13	ADR25020	Adr25020 Breast ca
	38	1332	96.3	2033	13	ADU06017	Adu06017 Novel bro
	39	1332	96.3	2033	14	ADX06366	Adx06366 Cyclin-de
	40	1332	96.3	2033	14	ADY15913	Ady15913 DNA encod
	41	1332	96.3	2033	14	ADY61794	Ady61794 Human gen
	42	1284	92.8	1500	6	ABT06285	Abt06285 Human NOV
	43	1044	75.5	1035	13	ADQ89833	Adq89833 Antagonis
	44	1044	75.5	1224	8	ACC51000	Acc51000 Human bla
	45	1044	75.5	1224	8	ABX76370	Abx76370 Lung canc

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 14, 2006, 21:18:18 ; Search time 878 Seconds  
(without alignments)  
2477.046 Million cell updates/sec

Title: US-10-601-011-1\_COPY\_126\_388  
Perfect score: 1383  
Sequence: 1 RQWALEDFEIGRPLGKGKFG.....SQRPMLREVLEHPWITANSS 263

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh  
-Q=/abss/ABSSWEB\_spool/US10601011/runat\_12022006\_150918\_13487/app\_query.fasta\_1  
-DB=Published\_Applications\_NA\_Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abss03h  
-USER=US10601011 @CGN\_1\_1\_1026 @runat\_12022006\_150918\_13487 -NCPU=6 -ICPU=3  
-NO\_MMAP -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published\_Applications\_NA\_Main:\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
4: /cgn2\_6/ptodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
6: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
8: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result			%				Description
	No.	Score	Match	Length	DB	ID	
	1	1383	100.0	2070	6	US-10-264-049-915	Sequence 915, App
	2	1383	100.0	2146	5	US-10-071-766-83	Sequence 83, Appl
	3	1383	100.0	2198	3	US-09-012-135A-2	Sequence 2, Appli
	4	1383	100.0	2198	3	US-09-784-332-2	Sequence 2, Appli
	5	1383	100.0	2198	8	US-10-734-126-2	Sequence 2, Appli
	6	1383	100.0	2237	6	US-10-240-965-252	Sequence 252, App
	7	1383	100.0	2253	6	US-10-172-118-929	Sequence 929, App
	8	1383	100.0	2253	6	US-10-388-360-323	Sequence 323, App
	9	1383	100.0	2253	6	US-10-295-027-989	Sequence 989, App
	10	1383	100.0	2253	7	US-10-342-887-929	Sequence 929, App
	11	1383	100.0	2253	7	US-10-188-832-34	Sequence 34, Appl
	12	1383	100.0	2253	8	US-10-751-736-2	Sequence 2, Appli
	13	1383	100.0	2253	8	US-10-781-581-186	Sequence 186, App
	14	1383	100.0	2253	9	US-10-848-755A-115	Sequence 115, App
	15	1383	100.0	2283	5	US-10-198-846-10281	Sequence 10281, A
c	16	1383	100.0	2284	3	US-09-814-353-21674	Sequence 21674, A
	17	1383	100.0	2347	5	US-10-209-324-1	Sequence 1, Appli
	18	1363	98.6	2148	6	US-10-240-965-251	Sequence 251, App
	19	1332	96.3	1209	9	US-10-745-237-261	Sequence 261, App
	20	1332	96.3	2033	6	US-10-172-118-881	Sequence 881, App
	21	1332	96.3	2033	7	US-10-342-887-881	Sequence 881, App
	22	1332	96.3	2033	9	US-10-848-755A-110	Sequence 110, App
	23	1332	96.3	2033	9	US-10-509-599-13	Sequence 13, Appl
	24	1284	92.8	1500	7	US-10-087-684-13	Sequence 13, Appl
	25	1284	92.8	1500	7	US-10-218-779-13	Sequence 13, Appl
	26	1044	75.5	1035	9	US-10-745-237-263	Sequence 263, App
	27	1044	75.5	1224	5	US-10-171-311-213	Sequence 213, App
	28	1044	75.5	1224	6	US-10-172-118-1004	Sequence 1004, Ap
	29	1044	75.5	1224	6	US-10-295-027-202	Sequence 202, App
	30	1044	75.5	1224	6	US-10-173-999-100	Sequence 100, App
	31	1044	75.5	1224	7	US-10-342-887-1004	Sequence 1004, Ap
	32	1044	75.5	1224	7	US-10-188-832-92	Sequence 92, Appl
	33	1044	75.5	1244	3	US-09-012-135A-1	Sequence 1, Appli
	34	1044	75.5	1244	3	US-09-784-332-1	Sequence 1, Appli
	35	1044	75.5	1244	8	US-10-734-126-1	Sequence 1, Appli
	36	1044	75.5	1261	8	US-10-335-053-258	Sequence 258, App
	37	1043	75.4	1168	3	US-09-920-300A-1709	Sequence 1709, Ap
	38	1043	75.4	1168	5	US-10-033-528-1709	Sequence 1709, Ap
	39	1043	75.4	1168	6	US-10-099-926-1709	Sequence 1709, Ap
	40	1043	75.4	1168	9	US-10-961-527-1709	Sequence 1709, Ap
	41	1032.5	74.7	1272	3	US-09-974-298-135	Sequence 135, App
	42	1032.5	74.7	1272	5	US-10-116-802-135	Sequence 135, App
	43	1032.5	74.7	1272	5	US-10-084-817-314	Sequence 314, App
	44	1031	74.5	1197	7	US-10-403-571-97	Sequence 97, Appl
	45	1031	74.5	1923	9	US-10-764-420-1670	Sequence 1670, Ap

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OM protein - protein search, using sw model

Run on: February 12, 2006, 18:58:35 ; Search time 43 Seconds  
(without alignments)  
588.489 Million cell updates/sec

Title: US-10-601-011-1\_COPY\_126\_388  
Perfect score: 1383  
Sequence: 1 RQWALED FEIGRPLGKGKFG.....SQRPMLREVLEHPWITANSS 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_80:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
1	1374	99.3	403	2	JC5974	aurora-related kin			
2	1292.5	93.5	395	2	JC5975	aurora-related kin			
3	1178	85.2	389	2	S52242	protein kinase (EC			
4	1174	84.9	407	2	S52243	p46Eg265 protein -			
5	1025	74.1	345	2	JC4665	protein kinase (EC			
6	933.5	67.5	282	2	H84653	probable protein k			
7	925.5	66.9	294	2	T10690	serine/threonine-s			
8	895.5	64.8	384	2	T41298	ser/thr protein ki			
9	891	64.4	421	2	A56220	protein kinase (EC			
10	890	64.4	305	2	T43221	serine/threonine-s			
11	890	64.4	329	2	B87790	protein B0207.4 [i			
12	858.5	62.1	288	2	T00862	probable serine/th			
13	769	55.6	326	2	T43219	serine/threonine-s			

14	769	55.6	343	2	D89124	protein K07C11.2 [
15	701.5	50.7	367	2	S47923	probable protein k
16	505	36.5	1650	2	T18444	hypothetical prote
17	501.5	36.3	465	2	B55748	protein kinase (EC
18	501.5	36.3	925	2	A55748	protein kinase (EC
19	493.5	35.7	440	2	T14735	probable serine/th
20	481	34.8	399	1	OKBYC1	protein kinase (EC
21	479.5	34.7	440	2	T14736	probable serine/th
22	477.5	34.5	441	2	C84667	probable protein k
23	475.5	34.4	480	2	A86427	probable serine/th
24	466	33.7	398	1	OKBYC3	protein kinase (EC
25	466	33.7	512	1	JC1446	serine/threonine-s
26	464	33.6	421	2	T48202	protein kinase AK2
27	464	33.6	461	2	T14822	probable serine/th
28	458.5	33.2	445	2	T50802	serine/threonine p
29	456.5	33.0	445	2	T09903	serine/threonine-s
30	452	32.7	442	2	T48203	hypothetical prote
31	452	32.7	489	2	T04862	probable serine/th
32	450	32.5	426	2	C71408	probable protein k
33	448	32.4	441	2	E85362	hypothetical prote
34	447.5	32.4	1398	2	T13741	hypothetical prote
35	446.5	32.3	746	2	S62365	SNF1-related prote
36	445	32.2	504	2	T10449	probable serine/th
37	445	32.2	511	1	A56009	serine/threonine-s
38	444.5	32.1	512	2	A54400	protein kinase (EC
39	443.5	32.1	301	1	A40811	myosin-light-chain
40	443.5	32.1	510	2	T04145	serine/threonine p
41	443	32.0	380	1	OKBYC2	protein kinase (EC
42	441	31.9	425	2	S41099	protein kinase (EC
43	440	31.8	481	2	JE0377	p70 S6 kinase (EC
44	439	31.7	648	1	JQ1150	protein kinase (EC
45	438	31.7	1245	2	D86260	protein T12C24.22



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OM protein - protein search, using sw model

Run on: February 12, 2006, 18:57:06 ; Search time 252 Seconds  
(without alignments)  
736.325 Million cell updates/sec

Title: US-10-601-011-1\_COPY\_126\_388  
Perfect score: 1383  
Sequence: 1 RQWALED FEIGRPLGKGKFG.....SQRPMLREVLEHPWITANSS 263

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_05.80:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1383	100.0	403	1	STK6_HUMAN	O14965 homo sapien
2	1334.5	96.5	405	2	Q4R1K4_PIG	Q4rlk4 sus scrofa
3	1310	94.7	397	1	STK6_RAT	P59241 rattus norv
4	1305	94.4	386	2	Q8C3H8_MOUSE	Q8c3h8 mus musculu
5	1305	94.4	395	1	STK6_MOUSE	P97477 mus musculu
6	1305	94.4	395	2	Q7TNK2_MOUSE	Q7tnk2 mus musculu
7	1294	93.6	395	2	Q8BP87_MOUSE	Q8bp87 mus musculu
8	1178	85.2	408	1	STK6L_XENLA	Q91819 xenopus lae
9	1176	85.0	408	2	Q6DJK0_XENLA	Q6djk0 xenopus lae
10	1174	84.9	407	1	STK6_XENLA	Q91820 xenopus lae
11	1174	84.9	407	2	Q6INY9_XENLA	Q6iny9 xenopus lae
12	1150	83.2	347	2	Q4R9G2_MACFA	Q4r9g2 macaca fasc
13	1146	82.9	343	2	Q5QPD5_HUMAN	Q5qpd5 homo sapien
14	1113	80.5	405	2	Q6DBZ4_BRARE	Q6dbz4 brachydanio
15	1075	77.7	367	2	Q4SS89_TETNG	Q4ss89 tetraodon n

16	1056	76.4	320	2	Q6NW76_BRARE	Q6nw76 brachydanio
17	1054	76.2	368	2	Q6GPL3_XENLA	Q6gpl3 xenopus lae
18	1051	76.0	361	2	Q9DF70_XENLA	Q9df70 xenopus lae
19	1047	75.7	361	2	Q8JG74_XENLA	Q8jg74 xenopus lae
20	1047	75.7	361	2	Q6DE08_XENLA	Q6de08 xenopus lae
21	1047	75.7	371	2	Q7ZYT9_XENLA	Q7zyt9 xenopus lae
22	1044	75.5	344	1	AURKB_HUMAN	Q96gd4 homo sapien
23	1031	74.5	344	2	Q7YRC7_PIG	Q7yrc7 sus scrofa
24	1031	74.5	345	1	AURKB_MOUSE	O70126 mus musculu
25	1031	74.5	345	2	Q8C6C1_MOUSE	Q8c6c1 mus musculu
26	1031	74.5	346	2	Q8JGS8_BRARE	Q8jgs8 brachydanio
27	1029	74.4	343	1	AURKB_RAT	O55099 rattus norv
28	1029	74.4	343	2	Q4V8N1_RAT	Q4v8n1 rattus norv
29	1025	74.1	344	2	Q7YRC6_BOVIN	Q7yrc6 bos taurus
30	1017	73.5	289	2	Q6AZY8_HUMAN	Q6azy8 homo sapien
31	1017	73.5	290	2	Q6DLZ0_HUMAN	Q6dlz0 homo sapien
32	1017	73.5	306	2	Q5Y191_HUMAN	Q5y191 homo sapien
33	1017	73.5	309	1	AURKC_HUMAN	Q9uqb9 homo sapien
34	1007	72.8	270	2	Q4RTH5_TETNG	Q4rth5 tetraodon n
35	963	69.6	276	2	Q6P209_MOUSE	Q6p209 mus musculu
36	963	69.6	282	1	AURKC_MOUSE	O88445 mus musculu
37	935.5	67.6	292	2	Q5SNH4_ORYSA	Q5snh4 oryza sativ
38	933.5	67.5	282	2	O82309_ARATH	O82309 arabidopsis
39	933.5	67.5	288	2	Q683C9_ARATH	Q683c9 arabidopsis
40	926	67.0	432	2	Q4R1K7_ORYSA	Q4r1k7 oryza sativ
41	925.5	66.9	294	2	Q9M077_ARATH	Q9m077 arabidopsis
42	924.5	66.8	294	2	Q8LBX4_ARATH	Q8lbx4 arabidopsis
43	913	66.0	404	2	Q7PY85_ANOGA	Q7py85 anopheles g
44	901	65.1	302	2	Q61XD3_CAEBR	Q61xd3 caenorhabdi
45	895.5	64.8	355	1	ARK1_SCHPO	O59790 schizosacch